There is currently great interest in harnessing non-sugar feedstocks for production of liquid fuels and value-added chemicals. One such example is to harness methane (a greenhouse gas) and convert it to liquid fuel (beginning with the activating step of making methanol). Synthesizing liquid fuel from methane is currently an expensive procedure that could alter both our environmental outlook and our fuel economy if it were achieved efficiently. To solve this problem, we are metabolically engineering *Methanococcus maripaludis S2*, a fast-growing methanogenic archaeon with well-developed genetic tools, to generate methanol from methane by inserting reaction pathways native to methanotrophic organisms. We have constructed a genome-scale metabolic model of *M. maripaludis* that allows us to predict the experimental outcomes of our engineering efforts and accounts for 477 of the 1722 protein coding genes (28%) in the *M. maripaludis* genome. Our model is the first for this organism to accurately depict the Wolfe cycle, the central catabolic pathway for methane and energy production in hydrogenotrophic methanogens that must function in reverse to achieve our proposed strain design. This model will provide a platform to generate designs for how to couple e.g. exergonic sulfate reduction pathways to make the ‘backwards’ use of methanogenic enzymes thermodynamically favorable. It is also the first model of any organism constructed using our likelihood-based gap filling approach, a method that we are currently expanding as a tool to make new fully-functional genome scale models by incrementally modifying existing models – all without ever ‘breaking’ their ability to simulate growth. Thus, this model represents both a vital piece of our work to modify *M. maripaludis* to efficiently convert methane to methanol and a first step toward the creation of a homology-based model morphing tool that will reduce the time and effort necessary to produce a high-quality genome scale model.

RELEVANT ACTIVITIES

In the box below, please indicate your particular activities which justify favorable consideration of you as a participant and contributor to this meeting.   
This information is important, as it allows the Scientific Organizers to make a thorough assessment when reviewing and selecting participants (max. 1700 characters).

I am a graduate student at the University of Illinois at Urbana-Champaign and conduct my research under Dr. Nathan Price at the Institute for Systems Biology (ISB) in Seattle, WA. Outside of my time in the research lab, I am highly active in education outreach efforts with the Valerie Logan Education Center at ISB and have worked with educators at both K-12 and community college levels. At the K-12 level, I serve as a scientific content expert to groups of 5-10 teachers and help the group design class lessons that conform to new Washington education standards. As part of my role, I supply examples of how concepts from each lesson can be applied in the real world and propose ways the teachers could bring these real world examples into their classrooms to get students excited about science. At the community college level, I have acted as a “big data mentor” to groups of teachers working to integrate big data concepts from systems biology into their curricula. In this role, I have helped assess critical ideas for big data science and suggested ways to make these ideas accessible to all students in their programs. I am also a member of the Editorial Board at ISB, a group of scientific researchers whose goal is to increase public awareness of the scientific advances at the institute. As a board member, I write short pieces aimed at a general audience that highlight recent publications by members of the institute and make the information accessible to individuals outside of the scientific community. These pieces describe research conducted by the Price lab and other groups at the institute and were published in ISB’s monthly newsletter, Molecular Me.